1010-92-74   **Teresa Haynes** and **Debra Knisley*** (`knisleyd@etsu.edu`), Mathematics Department, Box 70663, East Tennessee State University, Johnson City, TN 37614, and **Jeff Knisley** and **Yue Zou**. *Using graphical invariants to quantify secondary RNA structure.*

Determining the range of secondary RNA structural possibilities is an essential component of contemporary genomics research. The discovery of a diverse collection of transcripts that are involved in a large variety of processes has made it apparent that a complete understanding of intracellular processes is impossible without considering the role of RNA. While it is true that solutions based on thermodynamic parameters are known, it is not uncommon that the predicted minimum free energy structures are not the native ones. In this work, secondary RNA structures are represented as trees. Since trees have been highly studied as a family of graphs, we employ graphical invariants that are indicative of variations in the structure of trees. In particular, we utilize a number of domination parameters that are highly sensitive to the structural changes of small ordered trees in order to numerically characterize each tree. These parameters are used to train a back propagation artificial neural network to recognize the RNA-like trees from the non RNA-like trees. We demonstrate that a graphical analysis of the trees, without thermodynamic considerations, can determine which trees are RNA-like in structure. (Received August 23, 2005)

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